Variances in the expression profile of histaminergic system in the endometroid endometrial cancer

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Background:

Endometroid endometrial cancer (EC) is one of the most common malignant tumors in women. Research has indicated a higher concentration of histamine and polyamine in the endometroid tissue in comparison with healthy tissue.

Aim:

The aim of the study was to evaluate changes in the expression pattern of genes related histaminergic system in endometrial samples and whole blood in women with endometroid endometrial cancer.

Material and methods:

The study group consisted of 30 women with endometroid endometrial cancer qualified for hysterectomy (G1 well-differentiated, 15 cases; G2 moderately differentiated, eight cases; and G3 poorly differentiated, seven cases). The control group included 30 women with no neoplastic changes during routine gynecological examinations. The molecular analysis consisted of microarray analysis of genes related to the histaminergic systetem, and Reverse-Transcription Quantitative Polymerase Chain Reaction (RTqPCR). STATISTICA 13.3 PL software were used to the statistical analysis ($p < 0.05$).

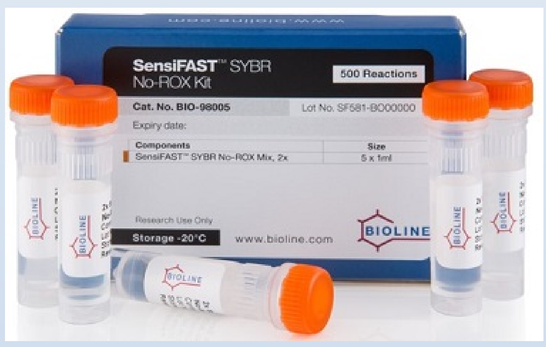

Fig. 1. SensiFast ™ SYBR No-ROX One-Step Kit (Bioline, London, UK) used to perform Reverse-Transcription Quantitative Polymerase Chain Reaction (RTqPCR) . [1]

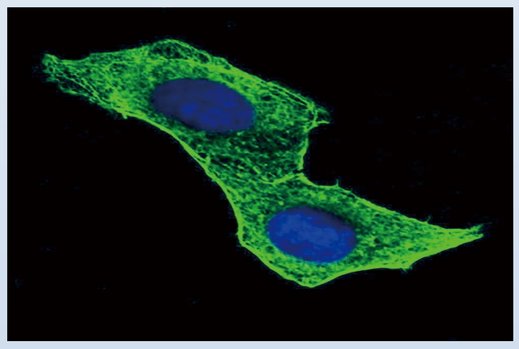

Fig. 2. Confocal immunofluorescent analysis of ACTB Antibody (Cat# 102-10055) with Hela cell followed by Alexa Fluor 488-conjugated goat anti-mouse lgG (green). DAPI was used to stain the cell nuclear (blue). [2]

Results:

It was shown that 10 from among 65 mRNAs connected with the histaminergic system differentiate the samples of tissue and blood obtained from patients with endometroid endometrial cancer in comparison with the control group ($p < 0.05$). It was observed that 2 mRNAs specifically differentiate samples G1 and G3 from the control, while gene 1 was distinctive for samples G3. On the other hand, HRH1, HRH3, and SLC23A2 were transcripts differentiating samples of endometroid endometrial cancer independent of either G or control. Along with the increase of the histopathological differentiation of the endometroid endometrial cancer the expression of the evaluated receptors was higher ($C<G1>G2>G3$; $p < 0.05$).

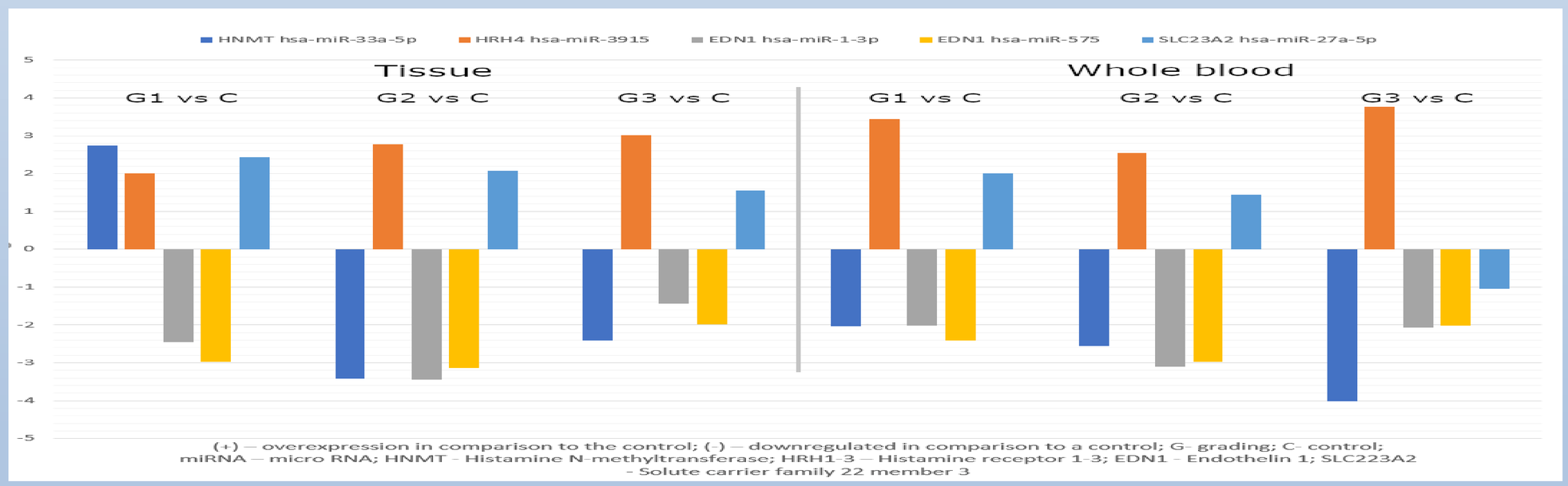

Fig. 3. Expression profile selected genes in endometrial tissue and whole blood of patients with endometrial cancer, compared to a control.

Conclusion:

The selected mRNAs seem to be promising as far as therapies targeted molecularly in the context of endometroid endometrial cancer.

Key words:

Histaminergic system, mRNA, endometroid endometrial cancer